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OM protein - protein search, using sw model

Run on: July 17, 2001, 16:55:27 ; Search time 37.5 seconds
(without alignments)
415.476 Million cell updates/sec

Title: US-09-403-724-5

Perfect score: 1415

Sequence: 1 CGLRLHRRQRRIIGKNSL.....PGVYTKVSFAFVPIKSVTKL 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
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6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1415	100.0	822	20 AAW99087	Human serine prote
2	1415	100.0	875	20 AAW83361	Human neurotrypsin
3	1298	91.7	761	20 AAW99088	Mouse serine prote
4	1298	91.7	761	20 AAW83362	Mouse neurotrypsin
5	467	33.0	526	11 AAR09227	t-PA deletion vari
6	463.5	32.8	437	10 AAR94410	Sequence of coding
7	463.5	32.8	483	16 AAR70890	Human tissue PA va
8	463.5	32.8	527	11 AAR06236	Novel tissue plasm
9	463.5	32.8	527	11 AAR09278	t-PA variant H432A
10	463.5	32.8	527	16 AAR70868	Human t-PA variant
11	463.5	32.8	527	16 AAR70903	Human t-PA variant

12	463.5	32.8	562	11 AAR04700	Sequence of tissue
13	462.5	32.7	525	11 AAR09230	t-PA deletion vari
14	462.5	32.7	562	9 AAP82582	Tissue plasminogen
15	462	32.7	356	19 AAW46917	Amino acid sequenc
16	462	32.7	526	11 AAR09228	t-PA deletion vari
17	462	32.7	1042	21 AAR09228	Human serine prote
18	461	32.6	296	21 AAY72108	Human serine prote
19	461	32.6	372	21 AAY72092	t-PA insertion var
20	461	32.6	528	11 AAR09216	Mouse Serine prote
21	461	32.6	1113	21 AAY44427	t-PA deletion vari
22	460	32.5	526	11 AAR09229	t-PA deletion vari
23	459.5	32.5	525	11 AAR09238	t-PA variant R449A
24	459.5	32.5	527	11 AAR09281	Human t-PA variant
25	459.5	32.5	527	16 AAR70871	Human t-PA variant
26	459.5	32.5	527	16 AAR70906	T-PA variant havin
27	459.5	32.5	559	12 AAR13154	Sequence of full l
28	459.5	32.5	562	4 AAP30001	T-PA variant havin
29	459.5	32.5	562	12 AAR12423	MB1083 t-PA varian
30	459.5	32.5	562	12 AAR13442	t-PA deletion vari
31	459	32.4	526	11 AAR09225	t-PA deletion vari
32	459	32.4	526	11 AAR09226	Human tissue PA va
33	458.5	32.4	483	16 AAR70889	Human tissue PA va
34	458.5	32.4	483	16 AAR79144	Human tissue PA va
35	458.5	32.4	483	16 AAR70884	Human tissue PA va
36	458.5	32.4	483	16 AAR70885	Human tissue PA va
37	458.5	32.4	483	16 AAR70886	Human tissue PA va
38	458.5	32.4	483	16 AAR70887	Human tissue PA va
39	458.5	32.4	483	16 AAR70888	Human tissue PA va
40	458.5	32.4	483	16 AAR70850	Human tissue PA va
41	458.5	32.4	483	16 AAR70852	Human tissue PA va
42	458.5	32.4	483	16 AAR70851	Human tissue PA va
43	458.5	32.4	483	16 AAR70853	Human tissue PA va
44	458.5	32.4	483	16 AAR70854	Human tissue PA va
45	458.5	32.4	483	16 AAR70855	Human tissue PA va

ALIGNMENTS

RESULT 1
AAW99087
ID: AAW99087 standard; Protein; 822 AA.
AC AAW99087;
XX
XX 13-MAY-1999 (first entry)
DT
XX Human serine protease BSSP-3.
DE
XX Serine protease; BSSP-3; brain tissue.
KW
XX Homo sapiens.
XX
XX WO9905290-A1.
XX
XX 04-FEB-1999.
XX
XX 24-JUL-1998; 98WO-JF03324.
XX
XX 24-JUL-1997; 97JP-0213969.
XX
XX (SUNR) SUNTORY LTD.

XX
XX Tsuruoka N, Yamaguchi N, Yamashiro K;
PI
XX WPI: 1999-142942/12.
DR
XX N-PSDB: AAX19024.
DR
XX
XX New serine protease expressed in brain tissue - used in screening
PT for potential serine protease inhibitors for drug use
PS Claim 1; Page 61-65; 69pp; Japanese.
XX

XX New serine protease expressed in brain tissue - used in screening
 PT for potential serine protease inhibitors for drug use
 XX
 XX Example 1; Page 51-54; 69pp; Japanese.
 XX
 CC The present sequence is a serine protease designated BSSP-3, which
 CC is isolated from mouse brain tissue. Transformants may be used to
 CC produce the enzyme or its partial sequences. Products from the present
 CC invention are used for screening for potential peptide or non-peptide
 CC serine protease inhibitors or expression regulators for use as drugs.
 XX
 XX Sequence 761 AA;
 XX

Query Match 91.7%; Score 1298; DB 20; Length 761;
 Best Local Similarity 90.3%; Pred. No. 7.4e-108;
 Matches 232; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 CGLRLHRRQKRIIGKNSLRGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 60
 DB 505 CGRLHRRQKRIIGKNSLRGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 564

QY 61 KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRPRDSYDIALVRLQGPPEQ 120
 DB 565 KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRPRDSYDIALVRLQGPPEQ 624

QY 121 CARFSSHVLPACLPWRPQKTASNCYITGWGDTGRAYSRITLQQAIIPLPKRFCEERY 180
 DB 625 CARLSTHVLPACLPWRPQKTASNCYITGWGDTGRAYSRITLQQAIIPLPKRFCKERY 684

QY 181 KGRFTGRMLCAGNLHEHKKRVDSGCGPLMCEPGEVWVYGVTSWGYCGVKDPSGV 240
 DB 685 KGLFTGRMLCAGNLHEHKKRVDSGCGPLMCEPGEVWVYGVTSWGYCGVKDPSGV 744

QY 241 YTKVSFAFVPWIKSVTKL 257
 DB 745 YTRVPFVPWIKSVTSL 761

RESULT 4
 AAW83362
 ID AAW83362 standard; Protein; 761 AA.
 XX
 AC AAW83362;
 XX
 DT 17-FEB-1999 (first entry)
 DE
 DE Mouse neurotrypsin.
 XX
 KW Mouse; neurotrypsin; tumour inhibition; neurological disease;
 KW lung disease; gene therapy; drug development; stroke; brain injury;
 KW neurodegeneration; neuroinflammatory disease; multiple sclerosis;
 KW epilepsy; hypoxia; ischaemia; nerve transection; neuroangiogenesis;
 KW emphysema; bronchitis.
 XX
 OS Mus musculus.
 XX
 PN WO9849322-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 24-APR-1998; 98WO-IB00625.
 XX
 PR 26-APR-1997; 97CH-0000966.
 XX
 PA (SOND/) SONDEREGGER P.
 XX
 PI Sonderegger P;
 XX
 DR WPI: 1999-009438/01.
 DR N-PSDB; AAV72590.
 XX

PT New human and murine neurotrypsin - used, e.g. for inhibiting
 PT tumours, treatment of neurological or lung disease, including by
 XX gene therapy and in drug development
 XX
 PS Claim 1; Page 29-32; 50pp; English.
 XX
 CC The present sequence represents mouse neurotrypsin. Neurotrypsin proteins
 CC and polynucleotides can be used: (i) to inhibit tumours, including
 CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage
 CC caused by stroke or brain injury (having a protective effect on the
 CC penumbra zone); (iii) to treat or prevent neurodegeneration.
 CC neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to
 CC increase survival of damaged neurons (e.g. in cases of hypoxia,
 CC ischaemia, nerve transection) and to stimulate regeneration and/or
 CC restoration of synapses; (v) to treat or prevent retinal disorders (e.g.
 CC degeneration or neovascularisation); (vi) to prevent apoptosis (or other
 CC causes of cell death) in the nervous system; (vii) to regenerate brain
 CC and/or nervous tissue; (viii) to treat pain; (ix) to improve brain
 CC performance, including learning and memory; (x) to treat or prevent a
 CC wide range of psychiatric disorders; and (xi) to treat brain or lung
 CC injury associated with protease expression (specifically emphysema or
 CC bronchitis).
 XX
 XX Sequence 761 AA;
 XX

Query Match 91.7%; Score 1298; DB 20; Length 761;
 Best Local Similarity 90.3%; Pred. No. 7.4e-108;
 Matches 232; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 CGLRLHRRQKRIIGKNSLRGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 60
 DB 505 CGRLHRRQKRIIGKNSLRGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 564

QY 61 KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRPRDSYDIALVRLQGPPEQ 120
 DB 565 KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRPRDSYDIALVRLQGPPEQ 624

QY 121 CARFSSHVLPACLPWRPQKTASNCYITGWGDTGRAYSRITLQQAIIPLPKRFCEERY 180
 DB 625 CARLSTHVLPACLPWRPQKTASNCYITGWGDTGRAYSRITLQQAIIPLPKRFCKERY 684

QY 181 KGRFTGRMLCAGNLHEHKKRVDSGCGPLMCEPGEVWVYGVTSWGYCGVKDPSGV 240
 DB 685 KGLFTGRMLCAGNLHEHKKRVDSGCGPLMCEPGEVWVYGVTSWGYCGVKDPSGV 744

QY 241 YTKVSFAFVPWIKSVTKL 257
 DB 745 YTRVPFVPWIKSVTSL 761

RESULT 5
 AAR09227
 ID AAR09227 standard; protein; 526 AA.
 XX
 AC AAR09227;
 XX
 DT 24-FEB-1993 (first entry)
 DE
 DE t-PA deletion variant d303.
 XX
 KW Tissue plasminogen activator; zymogen; clot; plasma; plasmin.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 302..303
 FT /label= deletion
 FT /note= "the amino acid at position 303 of the
 FT wild-type mature t-PA has been deleted"
 XX
 PN WO9002798-A.
 XX

FT Disulfide-bond 31..40
 FT Disulfide-bond 48..129
 FT Disulfide-bond 169..111
 FT Disulfide-bond 100..124
 FT Disulfide-bond 136..217
 FT Disulfide-bond 157..199
 FT Disulfide-bond 288..212
 FT Disulfide-bond 220..351
 FT Disulfide-bond 263..279
 FT Disulfide-bond 271..340
 FT Disulfide-bond 365..440
 FT Disulfide-bond 397..413
 FT Disulfide-bond 430..458
 FT Modified-site 73
 FT Modified-site 140
 FT Modified-site 404
 FT Modified-site 404
 FT /label= N-linked glycosylation site
 FT /label= N-linked glycosylation site
 FT /label= N-linked glycosylation site

XX US5385732-A.

XX 31-JAN-1995.

XX 20-MAY-1988; 88US-0196909.

XX 20-MAY-1988; 88US-0196909.

XX 15-FEB-1990; 90US-0480691.

XX 21-JAN-1992; 92US-0824740.

XX 22-MAR-1993; 93US-0035427.

XX (GETH) GENENTECH INC.

XX Anderson S, Brady KM, Keyt BA, Presta LG;

XX WPI; 1995-081536/11.

XX New tissue plasminogen activator variants - having an N-linked
 tripeptidyl glycosylation sequence inserted to increase plasma
 half-life

XX Claim 12; : 34pp; English.

XX The amino acid sequence of the human tissue plasminogen activator

XX (t-PA) variant delta1-44,N103,K210,E275,I277.

XX This sequence varies from the wild type sequence (AAR70842) by:

XX (a) a deletion of amino acids (AA) 1-44,

XX (b) substitution of AA at pos.: 103 - G to N; 210 - I to K; 275 - R to

XX E; 277 - K to I.

XX The numbers correspond to the residue positions in the wild type t-PA.

XX This sequence is one of a series of fibrinolytically active variant

XX t-PAs (see AAR70843-70908 + AAR79144). The variants are modified to

XX contain one or more amino acid substitutions, which provide an

XX Asn-X-Ser/Thr tripeptidyl sequence starting at the positions 57-61,

XX 63-69, 99, 101, 103-105, 106, 107, 109, 112, or 250 of the wild type t-PA

XX amino acid sequence. The Asn of the tripeptidyl sequence contains an

XX N-linked glycosylation site. The variant t-PAs exhibit fibrinolytic

XX activity and have longer half-lives and slower clearance rates from the

XX blood as compared to native t-PA. The variants can be used as

XX clot-dissolving agents in the treatment of vascular diseases or

XX conditions such as deep vein thrombosis or peripheral arterial

XX thrombosis.

QY 60 F-KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRDRSDYDIALVRLQGE 118
 Db 280 fgerf--pphltvlgtrvrvpgeeqkfevekyivhkefdddyndiallqlksds 337
 QY 119 EQCARFSSHVLPACLPL-----WRERPKTASNCYITGWD---TGRAYSRTLQQA 168
 Db 338 srcaqessvrtvcipadlqlpdwte-----ceisgygkhealspfyserikeahv 389
 QY 169 PLLPKRFCEERY--KGRFTGRMLCAG-----NLHEHKRVDSQCGDSGGLMCRPG 217
 Db 390 rlypsrctsqhllhhtvtdmclcagdttrsggppqanlh-----dacqgsgplvclndg 444
 QY 218 ESWVYGVTSWGYGCGVKDPSGYVTKVSAFVPMK 252
 Db 445 rmtlv-gliiswglcgqkdvpgvytkvtnylgdwir 478

RESULT 8

AAR06236

ID AAR06236 standard; protein; 527 AA.

XX AAR06236;

XX 11-DEC-1990 (first entry)

XX Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.

XX Fibrin; clotting; thrombolytic; vascular disease; stroke;

XX myocardial infarction; heart attack; pulmonary embolism; ds;

XX Homo sapiens.

XX EP379890-A.

XX 01-AUG-1990.

XX 10-JAN-1990; 90EP-0100457.

XX 23-JAN-1989; 89GB-0001422.

XX (FUJI) FUJISAWA PHARM KK.

XX Niwa M, Satoh S, Suzuki S, Otsuka K, Kusunoki C;

XX WPI; 1990-232757/31.

XX N-PSDB; AAQ05531.

XX New tissue plasminogen activator - having N-terminal peptide of

XX plasminogen linked to tissue plasminogen activator for increased

XX stability in vivo.

XX Disclosure; : p; English.

XX tPA with N-terminal peptide of plasminogen linked is more stable in

XX vivo than the native form. It is useful as a thrombolytic agent in

XX the treatment of vascular diseases eg myocardial infarction,

XX pulmonary embolism etc.

XX Sequence 527 AA;

XX Query Match 32.8%; Score 463.5; DB 11; Length 527;

XX Best Local Similarity 38.9%; Pred. No. 1.8e-33;

XX Matches 107; Conservative 41; Mismatches 88; Indels 39; Gaps 10;

QY 1 CGLRLHRRKRIIGKNSLRGGWPQVSLRLKSSHG-DG-RLLCGATLLSSCWLTAAHC 59

Db 264 cglrqsqpfriigllfadiashpwqaafakhrspgferlccgillsscwilsaahc 323

QY 60 F-KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQOIVIHREYRDRSDYDIALVRLQGE 118

Db 324 fgerf--pphltvlgtrvrvpgeeqkfevekyivhkefdddyndiallqlksds 381

PD 31-JAN-1995.
XX 20-MAY-1988; 88US-0196909.
XX 20-MAY-1988; 88US-0196909.
PR 15-FEB-1990; 90US-0480691.
PR 21-JAN-1992; 92US-0824740.
XX 22-MAR-1993; 93US-0035427.
XX (GETH) GENENTECH INC.
XX Anderson S, Brady KM, Keyt BA, Presta LG;
PI WPI; 1995-081536/11.
XX
XX New tissue plasminogen activator variants - having an N-linked
PT tripeptidyl glycosylation sequence inserted to increase plasma
PT half-life
XX
XX Claim 12; ; 34pp; English.
PS
XX The amino acid sequence of the human tissue plasminogen activator
CC (t-PA) variant N67,A432,A434.
CC This sequence varies from the wild type sequence (AAR70842) by
CC substitutions of AA at pos.: 67 - Y to N; 432 - H to A; 434 - R to A.
CC The numbers correspond to the residue positions in the wild type t-PA.
CC This sequence is one of a series of fibrinolytically active variant
CC t-PAs (see AAR70843-70908 + AAR79144). The variants are modified to
CC contain one or more amino acid substitutions, which provide an
CC Asn-X-Ser/Thr tripeptidyl sequence starting at the positions 57-61,
CC 63-69, 99, 101, 103-105, 106, 107, 109, 112, or 250 of the wild type t-PA
CC amino acid sequence. The Asn of the tripeptidyl sequence contains an
CC N-linked glycosylation site. The variant t-PAs exhibit fibrinolytic
CC activity and have longer half-lives and slower clearance rates from the
CC blood as compared to native t-PA. The variants can be used as
CC clot-dissolving agents in the treatment of vascular diseases or
CC conditions such as deep vein thrombosis or peripheral arterial
CC thrombosis.
XX
SQ Sequence 527 AA;

Query Match 32.8%; Score 463.5; DB 16; Length 527;
Best Local Similarity 38.9%; Pred. No. 1.8e-33;
Matches 107; Conservative 41; Mismatches 88; Indels 39; Gaps 10;

QY 1 CGLRLLRRQRRIIGGKNSLRGWPQVSLRLKSSHDGQ-RLICGATLLSCWVLTAAHC 59
Db 264 cglrqsqpfrikglfadiashpqaafakhrspgrflcggilisscwilsaahc 323

QY 60 F-KRYGNSTRSYAVRVGYHTLVPEEFEEETGVQOIVIHREYRDPDSYDIALVRLQPE 118
Db 324 fgerf--pphlvtlgrtyrvwpgeeqkfvekyivnkfeiddtdyndallqlksds 381

QY 119 EOCARFSSHLVPAQLPL-----WRERPORTASNCYITGWGD---TGRAYSRTLQQAAI 168
Db 382 sraaqessvrtvclppadlqlpdwte-----celsgyggkhealspfyserlkeav 433

QY 169 PLLPRFCEERY--KGRFTGRMLCAG-----NLHEHKKRVDSQCQDSGGLPMLCERP 217
Db 434 alypsarctsqhllnhtvtdmlcagdttrsppqanll-----dacqgdsppplvcindg 488

QY 218 ESMVVVGYTSMYCGVGDSPGVYTKVSFAVPWIK 252
Db 489 rmtlv-gliiswglgcgkdvpgvtykvtynidwir 522

RESULT 11
AAR70903
ID AAR70903 standard; Protein; 527 AA.
XX
AC AAR70903;
XX

DT 05-OCT-1995 (first entry)
XX Human t-PA variant (N103,A432,A434).
XX Human wild type tissue plasminogen activator; fibrinolytic; variant;
KW tripeptide; glycosylation site; half-life; clearance rate; blood;
KW clot-dissolving agent; vascular disease; thrombosis; artery; vein.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 1..44 /label= finger domain
FT Domain 45..91 /label= growth factor domain
FT Domain 92..173 /label= kringle 1 domain
FT Domain 180..261 /label= kringle 2 domain
FT Domain 264..527 /label= serine protease domain
FT Disulfide-bond 6..36
FT Disulfide-bond 34..43
FT Disulfide-bond 51..62
FT Disulfide-bond 56..73
FT Disulfide-bond 75..84
FT Disulfide-bond 92..173
FT Disulfide-bond 113..155
FT Disulfide-bond 144..168
FT Disulfide-bond 180..261
FT Disulfide-bond 201..243
FT Disulfide-bond 232..256
FT Disulfide-bond 264..395
FT Disulfide-bond 307..323
FT Disulfide-bond 315..384
FT Disulfide-bond 409..484
FT Disulfide-bond 441..457
FT Disulfide-bond 474..502
FT Modified-site 117 /label= N-linked glycosylation site
FT Modified-site 184 /label= N-linked glycosylation site
FT Modified-site 448 /label= N-linked glycosylation site
FT Modified-site 488 /label= N-linked glycosylation site
XX US5385732-A.
XX 31-JAN-1995.
XX 20-MAY-1988; 88US-0196909.
XX 20-MAY-1988; 88US-0196909.
PR 15-FEB-1990; 90US-0480691.
PR 21-JAN-1992; 92US-0824740.
PR 22-MAR-1993; 93US-0035427.
XX (GETH) GENENTECH INC.
XX Anderson S, Brady KM, Keyt BA, Presta LG;
XX WPI; 1995-081536/11.
XX New tissue plasminogen activator variants - having an N-linked
PT tripeptidyl glycosylation sequence inserted to increase plasma
PT half-life
XX
XX Claim 12; ; 34pp; English.
PS
XX The amino acid sequence of the human tissue plasminogen activator
CC (t-PA) variant N103,A432,A434.
CC This sequence varies from the wild type sequence (AAR70842) by
CC substitutions of AA at pos.: 103 - G to N; 432 - H to A; 434 - R to A.
CC The numbers correspond to the residue positions in the wild type t-PA.

XX 29-AUG-1989; 89WO-0909997.
 XX 24-JUL-1989; 89US-0384608.
 PR 02-SEP-1988; 88US-0240856.
 XX (GETH) GENENTECH INC.
 XX Anderson S, Bennett WE, Botstein D, Higgins DL, Paoni NF;
 PI Zoller M;
 XX WPI; 1990-115987/15.
 XX Modified tissue plasminogen activator - activated only when
 PT proximate to plasmin at site of clot and not systemically
 XX Claim 17; Page 43; 63pp; English.
 XX The t-PA variants represented in AAR09215-63 (and the T252R or N184S
 CC analogues thereof or combinations thereof) and AAR09266-83 have their
 CC fibrinolytic activity turned off when generally in the plasma and
 CC activated when proximate to plasmin at the site of the clot thus
 CC providing specific localised clot therapy.
 XX Sequence 525 AA;

Query Match 32.7%; Score 462.5; DB 11; Length 525;
 Best Local Similarity 39.1%; Pred. No. 2.4e-33;
 Matches 107; Conservative 42; Mismatches 86; Indels 39; Gaps 10;

QY 1 CGLRLHRRQKRIIGKNSLRGGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 60
 DB 264 cglrysqpfrikggfadiashpwwaafakrpsge-rfllcgillsscwllsaahcf 322
 QY 61 -KRYGNSTRSYAVRVGDYHTLVPEFEIEIGVQOVIHREYRPPDRSDYDIALVRLQGP 119
 DB 323 qerf--pphltvlgtrtyrvvpgeekfvekyivhkefdddyndiallqlksds 380
 QY 120 QCARFSSHVLPACLP-----WRERPKTASNCYITGWD---TGRAYSTLQQAIP 169
 DB 381 rcagessvrtvclpdpadlqlpdwte-----celsgyghkhealspfyserlkeahv 432
 QY 170 LLPKRFCEERY--KGRFTGRMLCAG-----NLHEHKRVDSQCGSGGGLMCRPGE 218
 DB 433 lypssrctsqhllnrtvtdnmlcagdtgrsggqanlh-----dacqgdsqgplvclndgr 487
 QY 219 SWVYGVTSWYGCYKSPGVYTKVSAFVPWIK 252
 DB 488 mtlv-gilswgigcgcgkdvpgvgtkvtynldwir 520

RESULT 14
 AAR2582
 ID AAR2582 standard; protein; 562 AA.
 XX
 AC AAR2582;
 XX
 DT 03-NOV-1990 (first entry)
 XX
 DE Tissue plasminogen activator with S-119 substd for M and QGI96-98
 DE substd for NGT.
 XX
 KW Modified tissue plasminogen activator; tPA; thrombosis; N-glycosylation.
 XX JP63230083-A.
 XX
 PD 26-SEP-1988.
 XX
 PF 20-MAR-1987; 87JP-0264339.
 XX
 PR 20-MAR-1987; 87JP-0264339.
 XX

PA (EISA) EISA KK.
 XX
 DR WPI; 1988-311961/44.
 XX N-PSDB; N825179.
 DR
 XX Modified tissue plasminogen activator - having glycine-183 and serine-186
 PT residues sustd. with serine and threonine.
 XX
 XX Disclosure; ; 16pp; Japanese.
 PS
 XX One N-glycosylation site, i.e. NSS (117-119) is substituted with
 CC NSM and the N-glycosylation is removed. Site 96-98 OGI is changed to
 CC NGT. Plasmid encoding the modified tPA is 99-6400 and its transformant
 CC is E.coli RRI-Zem 99-6400 (FERM P-9128).
 CC This modified tPA, used to treat thrombosis, is of high quality and
 CC has a longer half life period in blood.
 CC See also AAN82177-N82179.
 XX
 XX Sequence 562 AA;

Query Match 32.7%; Score 462.5; DB 9; Length 562;
 Best Local Similarity 38.9%; Pred. No. 2.4e-33;
 Matches 107; Conservative 41; Mismatches 88; Indels 39; Gaps 10;

QY 1 CGLRLHRRQKRIIGKNSLRGGWPQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCF 59
 DB 299 cglrysqpfrikggfadiashpwwaafakhrspggrfllcgillsscwllsaahc 358
 QY 60 F-KRYGNSTRSYAVRVGDYHTLVPEFEIEIGVQOVIHREYRPPDRSDYDIALVRLQGP 118
 DB 359 fgerf--pphltvlgtrtyrvvpgeekfvekyivhkefdddyndiallqlksds 416
 QY 119 EQCARFSSHVLPACLP-----WRERPKTASNCYITGWD---TGRAYSTLQQAIP 168
 DB 417 srcaqessvrtvclpdpadlqlpdwre-----celsgyghkhealspfyserlkeahv 468
 QY 169 LLPKRFCEERY--KGRFTGRMLCAG-----NLHEHKRVDSQCGSGGGLMCRPGE 217
 DB 469 rlypsrctsqhllnrtvtdnmlcagdtgrsggqanlh-----dacqgdsqgplvclndg 523
 QY 218 ESWYGVTSWYGCYKSPGVYTKVSAFVPWIK 252
 DB 524 rmtlv-gilswgigcgcgkdvpgvgtkvtynldwir 557

RESULT 15
 AAW46917
 ID AAW46917 standard; Peptide; 356 AA.
 XX
 AC AAW46917;
 XX
 DT 02-JUL-1998 (first entry)
 XX
 DE Amino acid sequence of a novel human kallikrein.
 XX
 KW Kallikrein; HKLP; human; serine protease; drug screening; antagonist;
 KW agonist; treatment; hypertension; cardiac hypertrophy; arthritis;
 KW inflammatory disorder; blood clotting disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 106 /note= "encoded by CRC"
 FT Misc-difference 168 /note= "encoded by YGG"
 FT
 XX WO9803665-A1.
 XX
 PD 29-JAN-1998.
 XX
 PF 21-JUL-1997; 97WO-US12724.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 17, 2001, 16:52:11 ; Search time 37.5 Seconds
(without alignments)
1414.560 Million cell updates/sec

Title: US-09-403-724-2
Perfect score: 4905
Sequence: 1 MTLARFVLMALMGALPEVVG.....PGVYTKVSFAFWIKSVTKL 875

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4905	100.0	875	20 AAW83361	Human neurotrypsin
2	4617	94.1	822	20 AAW99087	Human serine prote
3	3481	71.0	761	20 AAW95088	Mouse serine prote
4	3481	71.0	761	20 AAW83362	Mouse neurotrypsin
5	983.5	20.1	1785	19 AAW64591	Human SRCR protein
6	830	16.9	1436	22 AAB66088	Bovine WCI protein
7	822.5	16.8	1413	22 AAB66037	Human TANGO 234 ma
8	822.5	16.8	1453	22 AAB66037	Human TANGO 234
9	820.5	16.7	1319	22 AAB66040	Human TANGO 234 ex
10	690.5	14.1	1290	21 AAW07609	Rat von Ebner's gl
11	645.5	13.2	757	21 AAW19127	Polypeptide isolat

12	645	13.1	347	19	AAW64537	Human liver cell c
13	643	13.1	347	19	AAW68200	Human scavenger re
14	643	13.1	347	20	AAV13369	Amino acid sequenc
15	643	13.1	347	22	AAB80237	Human PRO229 prote
16	635	12.9	573	21	AAB49534	Clone HOEC84 #1.
17	598	12.2	774	21	AAB00077	Human lysyl oxidas
18	596	12.2	753	21	AAB00073	Human lysyl oxidas
19	591	12.0	641	21	AAB12307	Human secreted pro
20	591	12.0	754	21	AAB00078	Murine lysyl oxida
21	574	11.7	666	19	AAW64590	Human SRCR protein
22	564.5	11.5	1087	9	AAW80691	Hybrid plasminogen
23	559	11.4	1039	9	AAW80692	PA mutant Plg 1-54
24	558	11.4	807	13	AAW20013	Mouse Serine prote
25	545	11.1	1113	21	AAV44427	Tissue plasminogen
26	538.5	11.0	704	10	AAW90176	Human serine prote
27	528.5	10.8	1042	21	AAW44426	Human plasminogen.
28	525.5	10.7	791	18	AAW34285	Plasminogen mutein
29	523.5	10.7	812	12	AAW12948	Tissue plasminogen
30	522.5	10.7	794	10	AAW90179	Plasminogen mutein
31	521.5	10.6	812	12	AAW12934	Human 'glu' plasm
32	520.5	10.6	790	15	AAW60519	Sequence encoded b
33	520.5	10.6	810	14	AAW34428	Plasminogen protei
34	519.5	10.6	810	18	AAW31169	Plasminogen mutein
35	518.5	10.6	810	12	AAW12938	Plasminogen mutein
36	518	10.6	811	12	AAW12933	Plasminogen mutein
37	518	10.6	811	12	AAW12939	Plasminogen mutein
38	518	10.6	811	12	AAW12943	Plasminogen mutein
39	518	10.6	811	12	AAW12944	Plasminogen mutein
40	517.5	10.6	791	21	AAW01887	Human plasminogen
41	517.5	10.6	791	21	AAW99589	Human plasminogen
42	517.5	10.6	791	21	AAW50867	Human plasminogen
43	517.5	10.6	810	11	AAW08065	Human plasminogen
44	517.5	10.6	810	20	AAW08685	Human plasminogen
45	517.5	10.6	810	20	AAW02114	SEQ ID 77 of W0991

ALIGNMENTS

RESULT 1

AAW83361
ID AAW83361 standard; Protein; 875 AA.

XX AAW83361;

XX 17-FEB-1999 (first entry)

DT Human neurotrypsin.

DE Human neurotrypsin.

XX Human; neurotrypsin; tumour inhibition; neurological disease;

KW lung disease; gene therapy; drug development; stroke; brain injury;

KW neurodegeneration; neuroinflammatory disease; multiple sclerosis;

KW epilepsy; hypoxia; ischaemia; nerve transection; neovascularogenesis;

KW emphysema; bronchitis.

XX Homo sapiens.

OS Homo sapiens.

XX WO9849322-A1.

XX 05-NOV-1998.

XX 24-APR-1998; 98WO-IB00625.

XX 26-APR-1997; 97CH-0000966.

XX (SOND/) SONDEREGGER P.

XX Sonderegger P;

XX WPI; 1999-009438/01.

XX N-PSDB; AAW72589.

XX New human and murine neurotrypsin - used, e.g. for inhibiting

Db 121 ggnknefegtevyasvgtvcshddsdasvichqlqggkgiaktpfsglglipiy 180
 Qy 234 WSNVRCRDEENILLCEKDIWQGGVCPQKMAAAVTCFSHGTPFPPIRLAGSSVHEGRV 293
 Db 181 wsnvrcrgdeenillcekdikwggvcpqkmaaaavtcfsfshgtpfpilrlagssvhegrv 240
 Qy 294 ELYHAGOWGTVCDDQDDADADEVICRGLSGIAKAWHOAYFCGEGSPVMDDEVCTGNE 353
 Db 241 elyhagowgtvcddqddadaevicrqlgslgiakawhoayfgegspvmddevctgne 300
 Qy 354 LSIQCKSSWGEHNCGHKEDAGVSCPTLTDGVIRLAGGKSGHEGRLEVVYRGOWGTVCDD 413
 Db 301 lsiqcksswgehncghkedagvscptltdgvirlaggkshghegrlevvyrgowgtvcdd 360
 Qy 414 DGWTELTNYVVCRLGFKYKQASANHFESTGPIWLDDVSCSGKETRFQCSRRQGRH 473
 Db 361 dgwtehtnyvvcrlgfkylqasanhfestsipwldvscsgketrfqcsrrqgrh 420
 Qy 474 DCSHREDVSIACYPGEGHRLSLGFPVRLMDGENKKEGRVEVFINGOWGTICDDGTDKD 533
 Db 421 dcshtredvsiacypggeghrlslgfpvrlmdgenkkegrvevfingowgticddgtkd 480
 Qy 534 AAVICRQLGYKGPAPARTMAYFGEKGKGIHVDNVKCTGNERSLADCIKQDIGHNCRHSE 593
 Db 481 aavicrqlgykgapartmayfgekgkghivdnnvktgnersladcikqdgirhncrhse 540
 Qy 594 DAGVICYDFGKASGNSKNESLSSVCGRLRLHRRQKRIIGGKNSLRGGWPQVSLRLKSS 653
 Db 541 dagvicydfgkasgnsknslssvcgrlrlhrrqkrlilggknslrggwpqvslrlkss 600
 Qy 654 HGDGRLLCGATLLSSCWLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEFEEIGVQOIV 713
 Db 601 hgdgrllcgatllsscwltaaahcfkrygnstrsyavrvgyhtlvpeefeeigvqviv 660
 Qy 714 IHREYRPDRSDYDIALVRLQGPQECARFSSHVLPACILPWRERPKQTASNCYITGWGDT 773
 Db 661 ihreyrpdrrsdydialvrlqgpeeqcarfsshvlpacilpwrerpqktasncyitgwgt 720
 Qy 774 GRAYSRTLQQAALPLPRFCEERYKGRFTGRMLCAGNLHEHKKRVDSOCSGGPLMCEK 833
 Db 721 grayrtllqqaalplprfceerykgrftgrmlcagnlnehkrvdsocsggplmcer 780
 Qy 834 PGESWVYGVTSWVGCGVKDPSGYTKVSAFVPWIKSVTKL 875
 Db 781 pgeswvygvtswvgcgvkdpdsgytkvsafvpwvksvtkl 822

RESULT 3

AAW99088
 ID AAW99088 standard; Protein; 761 AA.

XX AAW99088;

XX 13-MAY-1999 (first entry)

XX Mouse serine protease BSSP-3.

XX Serine protease; BSSP-3; brain tissue.

XX Mus sp.

XX W09905290-A1.

XX 04-FEB-1999.

XX 24-JUL-1998; 98WO-JP03324.

XX 24-JUL-1997; 97JP-0213969.

XX (SUNR) SUNTORY LTD.

XX Tsuruoka N, Yamaguchi N, Yamashiro K;

XX WPI; 1999-142942/12.
 DR N-PSDB; AAX19027.
 XX New serine protease expressed in brain tissue - used in screening
 PT for potential serine protease inhibitors for drug use
 XX Example 1; Page 51-54; 69pp; Japanese.
 XX The present sequence is a serine protease designated BSSP-3, which
 CC is isolated from mouse brain tissue. Transforms may be used to
 CC produce the enzyme or its partial sequences. Products from the present
 CC invention are used for screening for potential peptide or non-peptide
 CC serine protease inhibitors or expression regulators for use as drugs.
 XX Sequence 761 AA:

Query Match 71.0%; Score 3481; DB 20; Length 761;

Best Local Similarity 71.8%; Pred. No. 9.9e-242;

Matches 628; Conservative 47; Mismatches 86; Indels 114; Gaps 4;

Qy 1 MTLARFVLAALMLGALPEVVGFDVSLNDSLHSHRHPAGPHYYPYLTQQRPPTRPP 60
 Db 1 mtlarfvlaalmlgalpevvgfdvslnslhshrhpagphyyypyltqqrpptrpp 54
 Qy 61 PLPRFPRPALPAQRPHALQAGHTPRPHWGPCPAGEPWSVTDGACPLRWAEVPPFLE 120
 Db 55 --prfplrpalpaqrphalqaghtprphwgcpagepwsvtdgacplrwaevpplle 112
 Qy 121 RSPASWALRGQRHFCRSPDAGRPWCYGDARKVDWGYCDCHRGSVRLRGKNEFE 180
 Db 113 rspaswaelrgqrhfcrspdagrpwcgydarkvdmgycdchrgsvrlrgknefe 157
 Qy 181 GTVEVYASVGMGTVCSSHWDSDASVICHQLGLGGKIAKQATPFGLGLIPIYWSNVR 240
 Db 158 ----- 157
 Qy 241 GDEENILLCEKDIWQGGVCPQKMAAAVTCFSHGTPFPPIRLAGSSVHEGRVLYHAG 300
 Db 158 -----gqpalpvlrvlggnsghegrvlyhag 186
 Qy 301 WGTVCDDQDDADADEVICRGLSGIAKAWHOAYFCGEGSPVMDDEVCTGNELSIEQCP 360
 Db 187 wgticddqddadaevicrqlgslgiakawhoayfgegspvmddevctgncelsieqcp 246
 Qy 361 KSSWGEHNCGHKEDAGVSCPTLTDGVIRLAGGKSGHEGRLEVVYRGOWGTVCDDGWTELN 420
 Db 247 ksswgehncghkedagvscptltdgvirlaggkshghegrlevvyrgowgtvcddgwteln 306
 Qy 421 TYVVCRLGFKYKQASANHFESTGPIWLDDVSCSGKETRFQCSRRQGRHDCSHRED 480
 Db 307 tyvacrlgfkylqasanhfestsipwldvscsgketrfqcsrrqgrhdcshred 366
 Qy 481 VSIACYPGEGHRLSLGFPVRLMDGENKKEGRVEVFINGOWGTICDDGWTDKDAVTCRQ 540
 Db 367 vsiacypggeghrlslgfpvrlmdgenkkegrvevfingowgticddgwtkdkaavtcrcq 426
 Qy 541 LGYKGPARTMAYFGEKGKGIHVDNVKCTGNERSLADCIKQDIGHNCRHSEADGVICD 600
 Db 426 lgykgapartmayfgekgkghivdnnvktgnersladcikqdgirhncrhseadgvlcd 486
 Qy 601 YFGKASGNSKNESLSSVCGRLRLHRRQKRIIGGKNSLRGGWPQVSLRLKSSHGDGRLL 660
 Db 486 yfgkasgnsknslssvcgrlrlhrrqkrlilggknslrggwpqvslrlksshgdgrll 546
 Qy 661 CGATLLSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEFEEIGVQOIVIHREYRP 720
 Db 546 cgatllscwvltaaahcfkrygnstrsyavrvgyhtlvpeefeeigvqvivihreyrp 606
 Qy 721 DRSDYDIALVRLQGPQECARFSSHVLPACILPWRERPKQTASNCYITGWGDTGRAYSRT 780
 Db 606 drsdydialvrlqgpeeqcarfsshvlpacilpwrerpqktasncyitgwgdtraysrt 666

KW autoantibody; ss.

OS Homo sapiens.

XX

PN WO9830687-A2.

XX

XX 16-JUL-1998.

PD

XX

PF 09-JAN-1998; 98WO-DE00096.

XX

PR 18-JUL-1997; 97DE-1030997.

XX

PR 09-JAN-1997; 97DE-1000519.

XX

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX

XX Mollenhauer J, Poustka A;

XX

XX WPI; 1998-399136/34.

DR

DR N-PSDB; AAV49652.

XX

XX Proteins containing scavenger receptor, cysteine rich domain -

XX

XX useful for diagnosis and treatment of tumours

PT

XX

XX Claim 2; Fig 2; 54pp; German.

XX

XX This sequence represents a human protein which contains a SRCR (scavenger

CC

CC receptor, cysteine-rich) domain. The gene and encoded protein can be used

CC

CC to diagnose or treat tumours, particularly of the nervous system

CC

CC (medullo-blastoma or glioma) or breast. The DNA sequence and probes

CC

CC derived from it, are used to identify genes that express SRCR-domain

CC

CC containing proteins, to determine the form in which these proteins exist

CC

CC and to assess the significance of individual forms on cellular

CC

CC properties. The protein can be used to detect the presence of

CC

CC autoantibodies and antibodies which regulate its expression.

XX

XX Sequence 1785 AA;

SQ

Query Match 20.1%; Score 983.5; DB 19; Length 1785;

Best Local Similarity 28.8%; Pred. No. 4.7e-62;

Matches 294; Conservative 92; Mismatches 353; Indels 283; Gaps 38;

QY 20 GFDSVL-----NDSLHSHRHSPAGPHYLYLPTQORPTTRPPPLPRFRPPRALPA 74

Db 434 gyesylwscphngwlnhcnqhsdag-----vicsaahswstpsptlptitpastvgs 488

QY 75 Q-----RPHALQAGHTPRPHMGCPAGEPWSVTFDGPCLR----WAE 114

Db 489 eeslallrvnggdrccgrvevlygg-----swgtvcddsw-dtndanvvcrgpgcgwam 541

QY 115 VPP-----FLERSPPASWALRGQRHNCFRSPDGAGRPW-----CFYGDARGKV- 158

Db 542 sapgnarfsgsgpplvldvrcsdhe-----sywscphngwlnhcnghsedagvic 593

QY 159 -----DMGYCDCRHGS-----VRLRGKNEFECTVEVYASGVMTVCSS 197

Db 594 sasqrtrpsptdw---ptshastagesslallrvnggdrccgrvevlyrgswgtvcdd 650

QY 198 HWDSDASVICHQLQGLGKGIKOTPFSS---GLGLIPIYWSNVRCDENILLCEKDIW 254

Db 651 ywtdndanvvcrgl---gcgwamsapgnarfsgsgpplvldvrcsdhesylwscphngw 707

QY 255 QGVCVCPKMAAAVTCFSHGTPFP-----IIRLAGGSSVHEGRVEL 295

Db 708 lshncghhedagvicasasqsgtptspdtwptshastagesslallrvnggdrccgrvev 767

QY 296 YHAGOMGTVCDDOWDDADEVICRQLGLSLGIAKAWHQAYFGEGSPVMLDEVRCGTNELS 355

Db 768 lyrgswgtvcdddywdndanvvcrglrgcwatsapgnarfsgsgpplvldvrcsdhesy 827

QY 356 IEQCPKSSWGEHNCGHKEDAGVSC-----TPLTGD-----VIRLAGGK 393

Db 828 lwschphngwlnhcnghhedagvicasasqsgtptspdtwptshastagesslallrvngg 887

QY 394 GSHEGRLEVYRGOMGTVCDDGWTTELNTYVVCROLGFKYKQASAN-HFEESTGPIWLDD 452

Db 888 drcgrvevlyrgswgtvcdddywdndanvvcrglrgcwamsapgnarfsgsgpplvldd 947

QY 453 VSCSKETRFLOCSRQWRHDCSHREDVSIACYPGGSE-----GHR 493

Db 948 vrcsdhesylwscphngwlnhcnghhedagvicasasqsgtprpdtwlttnlpaltvgs 1007

QY 494 LSLGFPVRLMDGENKKEGRVEVINGOMGTICDDGWTDKDAVICRQLGYGKPARARTMA 553

Db 1008 ssla--irlvnggdrccgrvevlyrgswgtvcddswtdndanvvcrglrgcwamsapgn 1065

QY 554 YFEGEGKPIHVDNKTGNERSLADCIKODIGRHNCRHSEDAGVIC-----DYFG 603

Db 1066 rfggsgpplvldvrcsdhesylwscphkgwlnhcnghhedagvicatqinstttdwh 1125

QY 604 KKASGNSKESLSSVCGLLRHRRQKRIIGG-----KNSLRGGWPQV----- 646

Db 1126 pttttarp---ssncggflfy-----asgtfsspsypayppnnakcvweievnsyri 1176

QY 647 -----SLRLKSSHG-----DGRLLCGATLLSSCWVLTAAHCFKRYGNSSTRSYAVRV 692

Db 1177 nlgsfnlkiahncsfdyveifdgslnslilgkic-----ndtrq--lft 1221

QY 693 GDYHTLVPEEFEEIGVQOIVIHREYRPRSDYDIALVRLQGPPEQCARFSSHVLPACLP 752

Db 1222 ssymrt-lhfrdisfngtflawynsfpsdatirlvlnssyglca----- 1268

QY 753 LWRERPKTASNCYIYG-WGDTGRAYSRTLOQAAIPLLPKRCFEERYKGRFTGRMLCAGN 811

Db 1269 -----grveiyhggtwg-tvcddswtqaeav-----vcrqlgcgravsai---gn 1310

QY 812 LHEHKRVDSQCQDGGGPL-----MCEPAGESWVYGVTSWVGCGVKDSP 856

Db 1311 ay-----fgsgsgpittlddvcsqstestlwqcrng--w-----fshncnhreda 1353

QY 857 GV 858

Db 1354 gv 1355

RESULT 6

AAB66088

ID AAB66088 standard; Protein; 1436 AA.

XX

AC AAB66088;

XX

DT 30-MAR-2001 (first entry)

XX

DE Bovine WC1 protein.

XX

KW Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;

KW central nervous system; focal brain disorder; bipolar affective disorder;

KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;

KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;

KW neuropsychiatric; psychoactive substance use; anxiety.

XX Bos sp.

XX WO200077239-A2.

PN

XX 21-DEC-2000.

XX

XX 24-MAY-2000; 2000WO-US14858.

XX

XX 14-JUN-1999; 99US-0333159.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;

XX

Db	1029	dahvvcqlgcvafnatvsahtgsgpwwldlndctgteshlwqcpargwghdcrhk	1088
Qy	373	EDAGVCTPLTDGVRIRLAGKGSHE--GRLEVYRQGWGTVCDDGWTELTNTYVVCRLGFG	430
Db	1089	edagvicesft--alrlysetetescagrlevfyngtwsgvgrnntaigivcrqlgc	1146
Qy	431	-KYGKQASANHFESTGPIWLDVSCGKETRFQCSRRQWGRHDCSHREDVSIACYPGG	489
Db	1147	gengvslaplsktgsgfmwvddiqcpkthislwqclsapwerriisspaeetwited--	1204
Qy	490	EGHRLSLGFPVRLMDGKNKKEGRVEVFINGQWGTICDDGWTDKDAAVICRLGYKGPARGA	549
Db	1205	-----rivrvggdtcsgrvelwhagwtvcdsdwlaeaeavvcqlgcgsalaa	1255
Qy	550	RTMAYFEGKGPIHVDNVKCTGNERSLADCIKODIGHNCRHSESDAGVICDYFGKASGN	609
Db	1256	lrdsafgggtgtlwdmrckgnesflwdchakpwgsgdchgedagvrc-----sq	1308
Qy	610	SNKE-----SLSSVCGLRLL-----HRRQKRIIGGKNSLRGGWPMQVSL	648
Db	1309	slkslnassghlalilssifglvllflwvltwcrvqkqkhl-----plrvt	1357
Qy	649	RLKSS 653	
Db	1358	rrrgs 1362	
RESULT	8		
ID	AAB66037	standard; Protein; 1453 AA.	
XX	AC	AAB66037;	
XX	DT	30-MAR-2001 (first entry)	
XX	DE	Human TANGO 234.	
XX	DE	TANGO protein; INTERCEPT protein; neurological disorder;	
KW	KW	central nervous system; focal brain disorder; bipolar affective disorder;	
KW	KW	global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;	
KW	KW	senile dementia; Huntington's disease; amyotrophic lateral sclerosis;	
KW	KW	Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;	
KW	KW	neuropsychiatric; psychoactive substance use; anxiety.	
XX	OS	Homo sapiens.	
XX	PN	WO200077239-A2.	
XX	PD	21-DEC-2000.	
XX	PF	24-MAY-2000; 2000WO-US14858.	
XX	PR	14-JUN-1999; 99US-0333159.	
XX	PA	(MILL-) MILLENNIUM PHARM INC.	
XX	PI	McCarthy SA, Fraser CC, Sharp JD, Barnes TM;	
XX	DR	WPI; 2001-032313/04.	
XX	DR	N-PSDB; AAF45123, AAF45124.	
XX	PT	TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for	
XX	PT	screening assays and diagnostic assays and for the treatment of	
XX	PT	neurological diseases such as Alzheimer's, Parkinson's and Huntington's	
XX	PT	disease -	
XX	PS	Claim 8; Fig 2; 359pp; English.	
XX	PS	The present invention relates to TANGO or INTERCEPT proteins and coding	
XX	CC	sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,	
XX	CC	AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding	
XX	CC	sequences are useful for the treatment of neurological disorders such as	
CC	CC	central nervous system (CNS) disorders, CNS-related disorders, focal	
CC	CC	brain disorders, global-diffuse cerebral disorders and other	
CC	CC	neurological and cerebrovascular disorders. The CNS disorders include	
CC	CC	Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic	
CC	CC	lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,	
CC	CC	autonomic function disorders such as hypertension and sleep disorders,	
CC	CC	neuropsychiatric disorders, psychoactive substance use disorders,	
XX	XX	anxiety, and bipolar affective disorder.	
XX	XX	Sequence 1453 AA;	
Qy	166	RHGSVRLRGKKEFEFTVEYASGVMTVCSSSHWDDSDASVICHOLQ-----LGGKGI	218
Db	896	rytdvrlvngksqcdgqvveinvlgwsgicdthwdpedarvicrlscgtalstggkyl	955
Qy	219	AKOTPFGLGLIPIYMSNVRCRDEENILLCEKDIWQGVCPQKMAAAVTCFSF-HGPTTF	277
Db	956	gers-----vrvvghrfhclgnesalldncqmtvlgappcihngntsvictgslqplf	1008
Qy	278	PI-----IRLAGSSVHEGRVELYHAGOWGTVCDDQWDDA	312
Db	1009	pclanvsvpysavpegasalicledkrlrlvldgdsrcaagrvelvdyhdfwticddgwdls	1068
Qy	313	DAEVICRLGLSLGIAKAWHOAYFEGSGVPMLDEVCTGNETSIEQCPKSSWGEHNCGHK	372
Db	1069	dahvvcqlgcvafnatvsahtgsgpwwldlndctgteshlwqcpargwghdcrhk	1128
Qy	373	EDAGVCTPLTDGVRIRLAGKGSHE--GRLEVYRQGWGTVCDDGWTELTNTYVVCRLGFG	430
Db	1129	edagvicesft--alrlysetetescagrlevfyngtwsgvgrnntaigivcrqlgc	1186
Qy	431	-KYGKQASANHFESTGPIWLDVSCGKETRFQCSRRQWGRHDCSHREDVSIACYPGG	489
Db	1187	gengvslaplsktgsgfmwvddiqcpkthislwqclsapwerriisspaeetwited--	1244
Qy	490	EGHRLSLGFPVRLMDGKNKKEGRVEVFINGQWGTICDDGWTDKDAAVICRLGYKGPARGA	549
Db	1245	-----rivrvggdtcsgrvelwhagwtvcdsdwlaeaeavvcqlgcgsalaa	1295
Qy	550	RTMAYFEGKGPIHVDNVKCTGNERSLADCIKODIGHNCRHSESDAGVICDYFGKASGN	609
Db	1296	lrdsafgggtgtlwdmrckgnesflwdchakpwgsgdchgedagvrc-----sq	1348
Qy	610	SNKE-----SLSSVCGLRLL-----HRRQKRIIGGKNSLRGGWPMQVSL	648
Db	1349	slkslnassghlalilssifglvllflwvltwcrvqkqkhl-----plrvt	1397
Qy	649	RLKSS 653	
Db	1398	rrrgs 1402	
RESULT	9		
ID	AAB66040	standard; Protein; 1319 AA.	
XX	AC	AAB66040;	
XX	DT	30-MAR-2001 (first entry)	
XX	DE	Human TANGO 234 extracellular domain.	
XX	KW	TANGO protein; INTERCEPT protein; neurological disorder;	
XX	KW	central nervous system; focal brain disorder; bipolar affective disorder;	
XX	KW	global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;	
XX	KW	senile dementia; Huntington's disease; amyotrophic lateral sclerosis;	
XX	KW	Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;	
XX	KW	neuropsychiatric; psychoactive substance use; anxiety.	

XX SQ Sequence 347 AA;

Query Match 13.1%; Score 643; DB 19; Length 347;
Best Local Similarity 40.0%; Pred. No. 1.8e-38;
Matches 138; Conservative 45; Mismatches 114; Indels 48; Gaps 10;

QY 280 IRLAGSSVHEGRVLYHAGOMGTVCDDQWDADAEVTCRQLGLSGIAKAWHQAYFGSGS 339
Db 24 vrlvgllhrcegrveqkgwtvcdgdgwdikdvaviclelqgc-----aasgtps 75
QY 340 G-----PVMLEVRCTGNELSTEQCPKSSWGHNCHEKEDAGVSC-----TP 381
Db 76 gilyeppaekedqllqsvstctgtdtlaqceee---vydshdedadascenpessfsp 133
QY 382 LTDGVIRLAGGSGHEGRLEVYRGOMGTVCDDGWTELTNTYVVCROLGFKYK-----QAS 437
Db 134 vpegv-rladgphckgrvevkhqpwytvctqgswlraakvvcrlqg--cgravltqkr 190
QY 438 ANHEESTGPIWLDVSCSGKETRFLOCSRRORGRHDCSHREDVSIACYPGCGEHLISIG 497
Db 191 cnkhaygrkpiwlsqmscsgreatlqdcpsgpgwknctnhdtdwtveced-----p 241
QY 498 FVRLMDGENKKEGRVEVFINGOMGTICDDGWTDKDAAVICRQLGYKGPARA---RTMAY 554
Db 242 fdrlrvvgdnlcsgrlevlhkgvsgvcdnwgkedqvckqlgc-gkslpsfdrkc 300
QY 555 FGEGKGPPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSESDAGVIC 599
Db 301 ypgvgriwldnvrscsgeeqsleqchrfwgfhdtchqedvavic 345

RESULT 14
AAV13369
ID AAY13369 standard; Protein; 347 AA.
XX AC AAY13369;
XX DT 25-JUN-1999 (first entry)
XX DE Amino acid sequence of protein PRO229.
XX KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophla areata;
KW anti-thrombotic; wound healing; tissue repair.
XX OS Homo sapiens.
XX PN WO9914328-A2.
XX PD 25-MAR-1999.
XX PF 16-SEP-1998; 98WO-US19330.
XX PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.

QY 555 FGEGKGPPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSESDAGVIC 599
Db 301 ypgvgriwldnvrscsgeeqsleqchrfwgfhdtchqedvavic 345

RESULT 13
AAW68200
ID AAW68200 standard; Protein; 347 AA.
XX AC AAW68200;
XX DT 07-DEC-1998 (first entry)
XX DE Human scavenger receptor protein SP alpha.
XX KW SP alpha; scavenger receptor; SRCR; human; antibody; immunoassay;
KW immunomodulator; autoimmune disease; transplant rejection;
KW infection; tumour; immunodeficiency; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT Protein 20..347
FT Protein /label= Mat_protein
FT Domain 24..125
FT /note= "cysteine-rich domain"
FT Domain 138..239
FT /note= "cysteine-rich domain"
FT Domain 245..346
FT /note= "cysteine-rich domain"

WO9839443-A1.
11-SEP-1998.
05-MAR-1998; 98WO-US04370.
06-MAR-1997; 97US-0039956.
(BRIM) BRISTOL-MYERS SQUIBB CO.
PI Aruffo AA, Gebe JA, Siadak AW;
XX WPI; 1998-495847/42.
XX N-PSDB; AAV54605.
XX New scavenger receptor cysteine-rich protein - the antibodies of
XX which can be used to modulate the immune response
XX Claim 7; Fig 1A-B; 46pp; English.
XX This is the amino acid sequence of a novel protein (see AAW68200),
CC termed SP alpha, that is a member of the scavenger receptor
CC cysteine-rich (SRCR) family. The sequence was deduced from an
CC isolated cDNA clone (see AAV54605). SP alpha transcripts are found
CC in human bone marrow, spleen, lymph node, thymus and foetal liver
CC but not in non-lymphoid tissues. SP alpha has the same domain
CC organisation as the extracellular region of CD5 and CD6 and is
CC composed of 3 SRCR domains. It is capable of binding to cells of
CC the monocytic lineage, and appears to be involved in the regulation
CC of monocyte activation, function and/or survival, and is therefore
CC an important component in the immunoregulatory system. Methods of
CC recombinantly producing SP alpha are disclosed. In addition,
CC antibodies reactive with SP alpha are provided, as are methods of
CC using antibodies that bind to SP alpha for modulating the
CC interaction between SPalpha and its receptor. SP alpha can be used
CC in pharmaceutical compositions to regulate the immune response in,
CC for example, autoimmune disease, viral infections, transplant
CC rejection suppression, tumour cell proliferation suppression, and
CC combined variable immunodeficiency.

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Job time: 196 sec